



STIC Search Report

Biotech-Chem Library

File Copy
10/006591
updated

STIC Database Tracking Number 154858

TO: David Lamberston
Location: REM-2B79/2C70
Art Unit: 1636
Friday, June 03, 2005

Case Serial Number: 10/006591

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Lamberston,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 303.378 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-8

Perfect score: 33

Sequence: 1 tttgtcacagattggctctgttcttgc 33

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues

Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications NA:*
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:*
 - 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
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 - 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
 - 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 - 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 - 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 33 | 100.0 | 33 | 14 | US-10-006-591-8 | Sequence 8, Appli |
| 2 | 33 | 100.0 | 59 | 14 | US-10-006-591-9 | Sequence 9, Appli |
| 3 | 33 | 100.0 | 59 | 14 | US-10-006-591-10 | Sequence 10, Appli |
| 4 | 33 | 100.0 | 681 | 18 | US-10-625-047-42 | Sequence 42, Appli |
| 5 | 33 | 100.0 | 681 | 18 | US-10-625-047-43 | Sequence 43, Appli |
| 6 | 33 | 100.0 | 681 | 18 | US-10-625-047-44 | Sequence 44, Appli |
| 7 | 33 | 100.0 | 681 | 18 | US-10-625-047-45 | Sequence 45, Appli |
| 8 | 33 | 100.0 | 681 | 18 | US-10-625-047-46 | Sequence 46, Appli |
| 9 | 33 | 100.0 | 681 | 18 | US-10-625-047-47 | Sequence 47, Appli |
| 10 | 33 | 100.0 | 681 | 19 | US-10-631-258-42 | Sequence 42, Appli |
| 11 | 33 | 100.0 | 681 | 19 | US-10-631-258-43 | Sequence 43, Appli |

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|------|----|-------|------|----|-------------------|--------------------|
| c 12 | 33 | 100.0 | 681 | 19 | US-10-631-258-44 | Sequence 44, Appli |
| c 13 | 33 | 100.0 | 681 | 19 | US-10-631-258-45 | Sequence 45, Appli |
| c 14 | 33 | 100.0 | 681 | 19 | US-10-631-258-46 | Sequence 46, Appli |
| c 15 | 33 | 100.0 | 681 | 19 | US-10-631-258-47 | Sequence 47, Appli |
| c 16 | 33 | 100.0 | 699 | 14 | US-09-740-002-17 | Sequence 8, Appli |
| c 17 | 33 | 100.0 | 1428 | 9 | US-09-740-002-18 | Sequence 17, Appli |
| c 18 | 33 | 100.0 | 1428 | 9 | US-09-740-002-19 | Sequence 19, Appli |
| c 19 | 33 | 100.0 | 1428 | 9 | US-09-335-697B-17 | Sequence 17, Appli |
| c 20 | 33 | 100.0 | 1428 | 9 | US-09-335-697B-19 | Sequence 19, Appli |
| c 21 | 33 | 100.0 | 1428 | 17 | US-10-384-356-17 | Sequence 17, Appli |
| c 22 | 33 | 100.0 | 1428 | 17 | US-10-384-356-19 | Sequence 19, Appli |
| c 23 | 33 | 100.0 | 1428 | 17 | US-10-325-698-17 | Sequence 17, Appli |
| c 24 | 33 | 100.0 | 1428 | 17 | US-10-325-698-19 | Sequence 19, Appli |
| c 25 | 33 | 100.0 | 1431 | 9 | US-09-758-173-3 | Sequence 3, Appli |
| c 26 | 33 | 100.0 | 1431 | 9 | US-09-758-173-11 | Sequence 11, Appli |
| c 27 | 33 | 100.0 | 1431 | 9 | US-09-948-429B-3 | Sequence 3, Appli |
| c 28 | 33 | 100.0 | 1431 | 9 | US-09-948-429B-11 | Sequence 11, Appli |
| c 29 | 33 | 100.0 | 1431 | 13 | US-10-124-905-3 | Sequence 3, Appli |
| c 30 | 33 | 100.0 | 1431 | 13 | US-10-124-905-11 | Sequence 11, Appli |
| c 31 | 33 | 100.0 | 1431 | 13 | US-10-073-138-2 | Sequence 2, Appli |
| c 32 | 33 | 100.0 | 1431 | 13 | US-10-073-138-6 | Sequence 6, Appli |
| c 33 | 33 | 100.0 | 1431 | 16 | US-10-124-807-3 | Sequence 3, Appli |
| c 34 | 33 | 100.0 | 1431 | 16 | US-10-124-807-11 | Sequence 11, Appli |
| c 35 | 33 | 100.0 | 1431 | 16 | US-10-291-532-3 | Sequence 3, Appli |
| c 36 | 33 | 100.0 | 1431 | 16 | US-10-291-532-11 | Sequence 11, Appli |
| c 37 | 33 | 100.0 | 1437 | 9 | US-09-758-173-7 | Sequence 7, Appli |
| c 38 | 33 | 100.0 | 1437 | 9 | US-09-948-429B-7 | Sequence 7, Appli |
| c 39 | 33 | 100.0 | 1437 | 13 | US-10-124-905-7 | Sequence 7, Appli |
| c 40 | 33 | 100.0 | 1437 | 13 | US-10-073-138-4 | Sequence 4, Appli |
| c 41 | 33 | 100.0 | 1437 | 16 | US-10-124-807-7 | Sequence 7, Appli |
| c 42 | 33 | 100.0 | 1437 | 16 | US-10-291-532-7 | Sequence 7, Appli |
| c 43 | 33 | 100.0 | 8530 | 9 | US-09-911-692-2 | Sequence 2, Appli |
| c 44 | 33 | 100.0 | 8540 | 9 | US-09-911-703-2 | Sequence 2, Appli |
| c 45 | 33 | 100.0 | 8540 | 12 | US-09-911-692-2 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-10-006-591-8
; Sequence 8, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GER
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description for Artificial Sequence: primer
US-10-006-591-8

Query Match 100.0%; Score 33; DB 14; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTTGTCAAGATTGGCTCTGCTTTCTGTC 33
Db 1 TTTGTCAAGATTGGCTCTGCTTTCTGTC 33

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 71.2689 Seconds
(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-8
Perfect score: 33
Sequence: 1 ttgtcacaagattggctctgtttctgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| C 1 | 33 | 100.0 | 687 | 1 | US-08-300-386A-1 |
| C 2 | 33 | 100.0 | 687 | 3 | US-08-931-645-1 |
| C 3 | 33 | 100.0 | 687 | 5 | PCT-US94-01258-1 |
| C 4 | 33 | 100.0 | 687 | 5 | PCT-US95-11235-1 |
| C 5 | 33 | 100.0 | 699 | 2 | US-08-480-753-1 |
| C 6 | 33 | 100.0 | 699 | 3 | US-08-041-889-8 |
| C 7 | 33 | 100.0 | 699 | 3 | US-08-837-058-8 |
| C 8 | 33 | 100.0 | 699 | 4 | US-09-417-264-8 |
| C 9 | 33 | 100.0 | 732 | 2 | US-08-480-753-3 |
| C 10 | 33 | 100.0 | 1418 | 3 | US-08-793-450-7 |
| C 11 | 33 | 100.0 | 1428 | 1 | US-08-488-376-17 |
| C 12 | 33 | 100.0 | 1428 | 1 | US-08-488-376-19 |
| C 13 | 33 | 100.0 | 1428 | 2 | US-08-634-223-17 |
| C 14 | 33 | 100.0 | 1428 | 2 | US-08-634-223-19 |
| C 15 | 33 | 100.0 | 1428 | 2 | US-08-634-224-17 |
| C 16 | 33 | 100.0 | 1428 | 2 | US-08-634-224-19 |
| C 17 | 33 | 100.0 | 1428 | 2 | US-08-634-400-17 |
| C 18 | 33 | 100.0 | 1428 | 2 | US-08-634-400-19 |
| C 19 | 33 | 100.0 | 1428 | 2 | US-08-635-878-17 |
| C 20 | 33 | 100.0 | 1428 | 2 | US-08-635-878-19 |
| C 21 | 33 | 100.0 | 1428 | 2 | US-08-770-057-17 |
| C 22 | 33 | 100.0 | 1428 | 2 | US-08-770-057-19 |
| C 23 | 33 | 100.0 | 1428 | 3 | US-09-335-697B-17 |
| C 24 | 33 | 100.0 | 1428 | 3 | US-09-335-697B-19 |
| C 25 | 33 | 100.0 | 1428 | 3 | US-09-335-697B-17 |
| C 26 | 33 | 100.0 | 1428 | 3 | US-09-335-697B-19 |
| C 27 | 33 | 100.0 | 1428 | 4 | US-09-740-002-17 |

| | | | | | |
|------|----|-------|------|---|------------------|
| C 28 | 33 | 100.0 | 1428 | 4 | US-09-740-002-19 |
| C 29 | 33 | 100.0 | 1431 | 3 | US-08-487-550-3 |
| C 30 | 33 | 100.0 | 1431 | 3 | US-08-487-550-11 |
| C 31 | 33 | 100.0 | 1431 | 4 | US-09-526-098-3 |
| C 32 | 33 | 100.0 | 1431 | 4 | US-09-526-098-11 |
| C 33 | 33 | 100.0 | 1431 | 4 | US-09-383-916-3 |
| C 34 | 33 | 100.0 | 1431 | 4 | US-09-383-916-11 |
| C 35 | 33 | 100.0 | 1437 | 3 | US-08-487-550-7 |
| C 36 | 33 | 100.0 | 1437 | 4 | US-09-526-098-7 |
| C 37 | 33 | 100.0 | 1437 | 4 | US-09-383-916-7 |
| C 38 | 33 | 100.0 | 4691 | 3 | US-08-591-632-43 |
| C 39 | 33 | 100.0 | 4691 | 3 | US-09-611-451-43 |
| C 40 | 33 | 100.0 | 6166 | 3 | US-08-591-632-51 |
| C 41 | 33 | 100.0 | 6166 | 3 | US-09-611-451-51 |
| C 42 | 33 | 100.0 | 8540 | 1 | US-08-149-099C-2 |
| C 43 | 33 | 100.0 | 8540 | 2 | US-08-478-967A-2 |
| C 44 | 33 | 100.0 | 8540 | 3 | US-08-475-815B-2 |
| C 45 | 33 | 100.0 | 8541 | 1 | US-08-476-275-1 |

ALIGNMENTS

RESULT 1

US-08-300-386A-1/c
; Sequence 1, Application US/08300386A
; Patent No. 5667988

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F.III
APPLICANT: Burton, Dennis R
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5667988th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/300,386A

FILING DATE: 02-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/174,674

FILING DATE: 28-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/826,623

FILING DATE: 27-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/012,566

FILING DATE: 02-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION/DOCKET NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 409.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 base pairs

TYPE: nucleic acid

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 / Search time 2021.32 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-8

Perfect score: 33
Sequence: 1 ttgtcacaagattgggtctgtcttctgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
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5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| C 1 | 31.4 | 95.2 | 240 | 2 | BE926107 QV3-BN014 |
| C 2 | 29.8 | 90.3 | 113 | 4 | BI000268 MR3-HN006 |
| C 3 | 29.8 | 90.3 | 137 | 1 | AA650442 n897H03.8 |
| C 4 | 29.8 | 90.3 | 140 | 2 | AW801185 |
| C 5 | 29.8 | 90.3 | 163 | 2 | AW797071 QV1-UM003 |
| C 6 | 29.8 | 90.3 | 163 | 2 | BE937481 RC4-ST027 |
| C 7 | 29.8 | 90.3 | 165 | 5 | BQ352204 MR3-HT073 |
| C 8 | 29.8 | 90.3 | 173 | 4 | BF990964 CMO-GN016 |
| C 9 | 29.8 | 90.3 | 186 | 2 | BF917580 IL3-UT011 |
| C 10 | 29.8 | 90.3 | 186 | 2 | BF917858 IL3-UT011 |
| C 11 | 29.8 | 90.3 | 186 | 4 | BI059720 IL3-UT011 |
| C 12 | 29.8 | 90.3 | 196 | 2 | AW796187 MR2-UM002 |
| C 13 | 29.8 | 90.3 | 205 | 2 | AW801000 MR3-UM005 |
| C 14 | 29.8 | 90.3 | 213 | 5 | BQ331892 P33-ET027 |
| C 15 | 29.8 | 90.3 | 216 | 2 | AW800122 MR2-UM006 |
| C 16 | 29.8 | 90.3 | 224 | 2 | AW800950 MR3-UM006 |
| C 17 | 29.8 | 90.3 | 233 | 2 | AW404463 UI-HF-BL0 |
| C 18 | 29.8 | 90.3 | 239 | 2 | AW380186 QV3-HT026 |
| C 19 | 29.8 | 90.3 | 249 | 2 | AW801076 MR3-UM005 |
| C 20 | 29.8 | 90.3 | 250 | 2 | AW610494 CM3-UM000 |
| C 21 | 29.8 | 90.3 | 251 | 2 | AW381136 CM4-HT029 |
| C 22 | 29.8 | 90.3 | 252 | 2 | AW800962 MR3-UM006 |
| C 23 | 29.8 | 90.3 | 254 | 2 | AW407471 UI-HF-BL0 |
| C 24 | 29.8 | 90.3 | 272 | 2 | BE931264 QV4-HT021 |

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| 26 | 29.8 | 90.3 | 275 | 4 | BI060115 IL3-UT011 |
| C 27 | 29.8 | 90.3 | 277 | 5 | BQ082613 K-BST0143 |
| C 28 | 29.8 | 90.3 | 278 | 4 | BM769216 K-BST0052 |
| 29 | 29.8 | 90.3 | 281 | 2 | AW800876 MR3-UM006 |
| 30 | 29.8 | 90.3 | 281 | 4 | BI004395 MR4-HN005 |
| C 31 | 29.8 | 90.3 | 289 | 2 | BF914949 IL3-UT011 |
| C 32 | 29.8 | 90.3 | 296 | 2 | AW800774 MR3-UM006 |
| C 33 | 29.8 | 90.3 | 300 | 2 | BF915089 IL3-UT011 |
| C 34 | 29.8 | 90.3 | 307 | 6 | CD702748 EST19273 |
| 35 | 29.8 | 90.3 | 312 | 5 | BQ376962 MR3-UM006 |
| C 36 | 29.8 | 90.3 | 313 | 4 | BG991608 MR3-HT039 |
| 37 | 29.8 | 90.3 | 316 | 2 | AW381559 PMI-HT030 |
| C 38 | 29.8 | 90.3 | 325 | 7 | T94543 Y636H02.r1 |
| C 39 | 29.8 | 90.3 | 328 | 2 | BE939719 CM4-UT000 |
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| 41 | 29.8 | 90.3 | 334 | 2 | BF914758 IL3-UT011 |
| 42 | 29.8 | 90.3 | 334 | 2 | BF914818 IL3-UT011 |
| 43 | 29.8 | 90.3 | 337 | 2 | BF915921 IL3-UT011 |
| C 44 | 29.8 | 90.3 | 337 | 2 | BF837357 PM3-HT035 |
| C 45 | 29.8 | 90.3 | 340 | 2 | AW792987 CM3-UM000 |

ALIGNMENTS

RESULT 1
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LOCUS BE926107 240 bp mRNA linear EST 02-OCT-2000
DEFINITION QV3-BN0149-220800-300-b06 BN0149 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE926107
VERSION BE926107.1 GI:10452183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 240)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=QV3-BN0149-220800-300-b06&t3=2000-08-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 240.
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1. 240
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0149"
/note="Organ: breast normal; Vector: puc18; Site: 1: Smai; Site_2: Smai; A mini-library was made by cloning products

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 243.756 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-8
Perfect score: 33
Sequence: 1 ttgtcacagattgggtctgtcttctgtc 33

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
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| 4 | 33 | 100.0 | 681 | 13 ADQ98065 | Adq98065 Chimeric |
| 5 | 33 | 100.0 | 681 | 13 ADQ98066 | Adq98066 Chimeric |
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| 8 | 33 | 100.0 | 681 | 13 ADQ98069 | Adq98069 Chimeric |
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| 11 | 33 | 100.0 | 699 | 2 AAT44088 | Aat44088 Ulcerativ |
| 12 | 33 | 100.0 | 699 | 2 ADE51514 | Ades51514 p-ANCA re |
| 13 | 33 | 100.0 | 699 | 2 AAV51394 | Aav51394 UC PANCA |
| 14 | 33 | 100.0 | 699 | 2 AAX91122 | Aax91122 NANUC-2 a |
| 15 | 33 | 100.0 | 699 | 2 AAZ90667 | Aaz90667 UC PANCA |
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| 17 | 33 | 100.0 | 732 | 2 ADE51516 | Ades51516 p-ANCA re |
| 18 | 33 | 100.0 | 732 | 2 AAV51396 | Aav51396 UC PANCA |
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| C 44 | 33 | 100.0 | 2349 | 12 | ADP44636 | Adp44636 Human ant |
| C 45 | 33 | 100.0 | 4691 | 2 | AAQ92546 | Aaq92546 Murine an |

ALIGNMENTS

RESULT 1
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ID ABN84084 standard; DNA; 33 BP.
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AC ABN84084;
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DT 23-SEP-2002 (first entry)
XX
DE Heavy chain CH1 constant region primer.
XX
KW Antibody; pRL5-CAT; vector; primer; ss.
XX
OS Unidentified.
XX
PN WO200246435-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047452.
XX
PR 05-DEC-2000; 2000US-0251440P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
PI McWhirter J;
XX
DR WPI; 2002-537569/57.
XX
PT Plasmid for in situ production of genes, comprises two template annealing
PT sequences, such as downstream primer and upstream collar sequence and a
PT restriction site located between the annealing sequences.
XX
PS Claim 34; Page 19; 65pp; English.
XX
CC The present sequence is a heavy chain CH1 constant region primer that is
CC used in the engineering of plasmids of the invention, especially plasmid
CC pRL5-CAT (see ABN84078), for the in situ production of genes. It was
CC found nucleic acids encoding at least a portion of an antibody can be
CC directly incorporated into a plasmid by reverse transcription of mRNA.
CC The plasmid is engineered into a template annealing sequences, i.e.
CC a downstream primer that anneals to a first portion of a nucleic acid
CC template, e.g. mRNA encoding at least a portion of an antibody, and an

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 823.336 Seconds
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1942.126 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 6: gb.pat.*
- 7: gb.ph.*
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- 11: gb.sts.*
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- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 9 | 33 | 100.0 | 732 | 6 | AR051552 Sequence |
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| 11 | 33 | 100.0 | 1413 | 6 | AX709548 Sequence |
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LOCUS AX642156 33 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8 from Patent WO0246435.
ACCESSION AX642156
VERSION AX642156.1 GI:28474644

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Bowdish, K.S., Barbas-Frederickson, S., Lin, Y.C., Renshaw, M., Wild, M. and McWhirter, J.

TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0246435-A 8 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)

FEATURES
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description for Artificial Sequence: primer"

ORIGIN

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGTGTCACAGATTGGGCTCTGCTTCTTGTGTC 33
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Db 1 TTGTGTCACAGATTGGGCTCTGCTTCTTGTGTC 33

RESULT 2

LOCUS AX642157 59 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9 from Patent WO0246435.
ACCESSION AX642157
VERSION AX642157.1 GI:28474645

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 183.866 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-7
Perfect score: 20
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues
Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 5 | 19 | 95.0 | 20 | US-10-738-120-25 |
| 6 | 19 | 95.0 | 21 | US-10-920-899-1320 |
| 7 | 19 | 95.0 | 21 | US-10-920-899-1408 |
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| c 14 | 19 | 95.0 | 23 | 10 | US-09-939-769-7 | Sequence 7, Appl |
| c 15 | 19 | 95.0 | 23 | 10 | US-09-833-041-36 | Sequence 36, Appl |
| c 16 | 19 | 95.0 | 23 | 11 | US-09-833-245-36 | Sequence 36, Appl |
| c 17 | 19 | 95.0 | 23 | 11 | US-09-832-929-36 | Sequence 36, Appl |
| c 18 | 19 | 95.0 | 23 | 14 | US-10-077-023-121 | Sequence 121, Appl |
| c 19 | 19 | 95.0 | 23 | 14 | US-10-075-846-38 | Sequence 38, Appl |
| c 20 | 19 | 95.0 | 23 | 14 | US-10-056-884-31 | Sequence 31, Appl |
| c 21 | 19 | 95.0 | 23 | 14 | US-10-080-980-28 | Sequence 28, Appl |
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| c 23 | 19 | 95.0 | 23 | 14 | US-10-086-156-58 | Sequence 58, Appl |
| c 24 | 19 | 95.0 | 23 | 14 | US-10-081-775-28 | Sequence 28, Appl |
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| c 26 | 19 | 95.0 | 23 | 14 | US-10-067-443-33 | Sequence 33, Appl |
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| c 30 | 19 | 95.0 | 23 | 15 | US-10-067-800-23 | Sequence 23, Appl |
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| c 33 | 19 | 95.0 | 23 | 15 | US-10-071-458-40 | Sequence 40, Appl |
| c 34 | 19 | 95.0 | 23 | 15 | US-10-116-519-105 | Sequence 105, Appl |
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| c 40 | 19 | 95.0 | 23 | 16 | US-10-210-152-270 | Sequence 270, Appl |
| c 41 | 19 | 95.0 | 23 | 16 | US-10-234-951A-26 | Sequence 26, Appl |
| c 42 | 19 | 95.0 | 23 | 16 | US-10-135-839-23 | Sequence 23, Appl |
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ALIGNMENTS

RESULT 1
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; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN.
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
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US-10-006-591-7

Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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SUMMARIES

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| C 40 | 19 | 95.0 | 235 | 4 | US-09-513-999C-66 | Sequence 66, Appl |
| C 41 | 19 | 95.0 | 240 | 3 | US-07-987-264-17 | Sequence 17, Appl |
| C 42 | 19 | 95.0 | 301 | 4 | US-09-513-999C-71 | Sequence 71, Appl |
| C 43 | 19 | 95.0 | 354 | 2 | US-08-652-816A-21 | Sequence 21, Appl |
| C 44 | 19 | 95.0 | 354 | 2 | US-08-428-257A-77 | Sequence 77, Appl |
| C 45 | 19 | 95.0 | 354 | 3 | US-07-987-264-59 | Sequence 59, Appl |

ALIGNMENTS

RESULT 1

US-08-211-202-30/c
; Sequence 30, Application US/08211202
; Patent No. 5565332

GENERAL INFORMATION:

APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIER, Michael
APPLICANT: JESSERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60605-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: -US/08/211,202
FILING DATE: 23-SEP-1992
APPLICATION NUMBER: GB 9120252.3
PRIORITY DATE: 23-SEP-1991
PRIORITY APPLICATION DATA:
FILING DATE: 25-SEP-1991
APPLICATION NUMBER: GB 9120377.8
PRIORITY DATE: 24-MAR-1992
APPLICATION NUMBER: GB 9206318.9
PRIORITY DATE: 24-MAR-1992
PRIORITY APPLICATION DATA:
FILING DATE: 25-SEP-1991
APPLICATION NUMBER: GB 9206372.6
PRIORITY DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 1225.04 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20

Sequence: 1 gactgcaccagctgnacctg 20

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 2 | 19 | 95.0 | 226 | 2 | AW505280 UI-HF-BMO |
| C 3 | 19 | 95.0 | 231 | 2 | AW382578 CMO-HT033 |
| C 4 | 19 | 95.0 | 234 | 5 | BQ084534 K-EST0149 |
| C 5 | 19 | 95.0 | 238 | 7 | T29670 EST89669 Hu |
| C 6 | 19 | 95.0 | 244 | 2 | AW403100 UI-HF-BMO |
| C 7 | 19 | 95.0 | 264 | 2 | AW403531 UI-HF-BMO |
| C 8 | 19 | 95.0 | 279 | 1 | AA300571 EST13661 |
| C 9 | 19 | 95.0 | 282 | 8 | B73518 CIT-HSP-857 |
| C 10 | 19 | 95.0 | 300 | 1 | AU098611 AU098611 |
| C 11 | 19 | 95.0 | 300 | 1 | AU098624 AU098624 |
| C 12 | 19 | 95.0 | 302 | 2 | AW403015 UI-HF-BMO |
| C 13 | 19 | 95.0 | 302 | 2 | AW607003 RC3-HT044 |
| C 14 | 19 | 95.0 | 305 | 2 | AW402911 UI-HF-BMO |
| C 15 | 19 | 95.0 | 306 | 2 | AW402857 UI-HF-BMO |
| C 16 | 19 | 95.0 | 306 | 2 | AW403516 UI-HF-BMO |
| C 17 | 19 | 95.0 | 312 | 2 | AW401829 UI-HF-BMO |
| C 18 | 19 | 95.0 | 321 | 2 | AW130201 xF29h05.x |
| C 19 | 19 | 95.0 | 331 | 2 | AW407729 UI-HF-BMO |
| C 20 | 19 | 95.0 | 341 | 2 | BF128876 601811064 |
| C 21 | 19 | 95.0 | 344 | 2 | AW403535 UI-HF-BMO |
| C 22 | 19 | 95.0 | 359 | 2 | BE010378 CMO-BN018 |
| C 23 | 19 | 95.0 | 364 | 2 | AW380763 CMO-HT028 |
| C 24 | 19 | 95.0 | 381 | 4 | BM798753 K-EST0082 |

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| C 25 | 19 | 95.0 | 388 | 2 | BE170030 | BE170030 CM4-HT053 |
| C 26 | 19 | 95.0 | 388 | 2 | BE170043 | CM4-HT053 |
| C 27 | 19 | 95.0 | 391 | 2 | BF154501 | PMO-BN017 |
| C 28 | 19 | 95.0 | 396 | 2 | AW402942 | UI-HF-BMO |
| C 29 | 19 | 95.0 | 402 | 6 | CD686221 | EST2742 H |
| C 30 | 19 | 95.0 | 403 | 1 | AB107217 | AB107217 |
| C 31 | 19 | 95.0 | 407 | 6 | CD705186 | CD705186 |
| C 32 | 19 | 95.0 | 412 | 2 | AW951843 | EST363913 |
| C 33 | 19 | 95.0 | 416 | 2 | AW402457 | UI-HF-BMO |
| C 34 | 19 | 95.0 | 416 | 8 | AQ056004 | CIT-HSP-2 |
| C 35 | 19 | 95.0 | 417 | 2 | AW408371 | UI-HF-BMO |
| C 36 | 19 | 95.0 | 418 | 2 | AW401468 | UI-HF-BMO |
| C 37 | 19 | 95.0 | 419 | 2 | AW402189 | UI-HF-BMO |
| C 38 | 19 | 95.0 | 429 | 2 | AW630630 | h85d11.Y |
| C 39 | 19 | 95.0 | 435 | 5 | EX480340 | DKF20686K |
| C 40 | 19 | 95.0 | 448 | 2 | AW402665 | UI-HF-BMO |
| C 41 | 19 | 95.0 | 454 | 2 | BF238165 | BF238165 |
| C 42 | 19 | 95.0 | 455 | 4 | BG745555 | 602723953 |
| C 43 | 19 | 95.0 | 457 | 2 | AW405627 | UI-HF-BMO |
| C 44 | 19 | 95.0 | 458 | 2 | BE169081 | PM3-HT052 |
| C 45 | 19 | 95.0 | 460 | 2 | AW406939 | UI-HF-BMO |

ALIGNMENTS

RESULT 1
AW408784/C

LOCUS

DEFINITION

AW408784

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AW408784 194 bp mRNA linear EST 16-FEB-2000
UI-HF-BMO-adv-b-10-0-UI.r1 NIH_MGC_38 Homo sapiens cDNA clone
IMAGE:3063115 5', mRNA sequence.

AW408784.1 GI:6927841

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-x@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html

Seq primer: M13 Forward.

Location/Qualifiers

1..194

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3063115"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (LTI)"

/clone_lib="NIH MGC 38"

/notes="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(2.5-3.5kb). Directionally cloned. Cells provided by Louis

M. Staudt, Ph.D. Library preparation by Maria de Fatima

Ronaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match

Best Local Similarity

95.0%; Score 19; DB 2; Length 194;

95.0%; Pred. No. 4.8e+02;

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 147.731 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20
Sequence: 1 gactgcaccagctgnacctg 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
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| C 2 | 19 | 95.0 | 20 | 8 | ACC44845 |
| C 3 | 19 | 95.0 | 20 | 12 | ADQ39458 |
| C 4 | 19 | 95.0 | 20 | 12 | ADQ75790 |
| C 5 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 6 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 7 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 8 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 9 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 10 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 11 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 12 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 13 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 14 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 15 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 16 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 17 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 18 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 19 | 19 | 95.0 | 20 | 13 | ADQ75790 |
| C 20 | 19 | 95.0 | 20 | 13 | ADQ75790 |

| | | | | | | |
|------|----|------|----|---|----------|--------------------|
| C 21 | 19 | 95.0 | 23 | 4 | ABN87303 | Abn87303 Human VH |
| C 22 | 19 | 95.0 | 23 | 6 | ABK51871 | Abk51871 PCR prime |
| C 23 | 19 | 95.0 | 23 | 6 | ABK76645 | Abk76645 Novel met |
| C 24 | 19 | 95.0 | 23 | 6 | ADQ28816 | Adq28816 Human ant |
| C 25 | 19 | 95.0 | 23 | 6 | ABQ82761 | Abq82761 K+betaM3 |
| C 26 | 19 | 95.0 | 23 | 6 | ABK68571 | Abk68571 Human imm |
| C 27 | 19 | 95.0 | 23 | 6 | ABQ83143 | Abq83143 Human HGP |
| C 28 | 19 | 95.0 | 23 | 6 | ABT09822 | Abt09822 K+beta M6 |
| C 29 | 19 | 95.0 | 23 | 6 | ABK93295 | Abk93295 PCR prime |
| C 30 | 19 | 95.0 | 23 | 6 | ADQ42427 | Adq42427 Human HDG |
| C 31 | 19 | 95.0 | 23 | 6 | ADQ46080 | Adq46080 Human K+b |
| C 32 | 19 | 95.0 | 23 | 6 | ADQ30847 | Adq30847 PCR prime |
| C 33 | 19 | 95.0 | 23 | 6 | ADQ49667 | Adq49667 Anti-HGPR |
| C 34 | 19 | 95.0 | 23 | 6 | AAK98426 | Aak98426 Human V g |
| C 35 | 19 | 95.0 | 23 | 6 | AAK98467 | Aak98467 Human V g |
| C 36 | 19 | 95.0 | 23 | 6 | ADJ33351 | Adj33351 Human VH |
| C 37 | 19 | 95.0 | 23 | 8 | ABT42678 | Abt42678 Human GPC |
| C 38 | 19 | 95.0 | 23 | 8 | AAU59939 | Aau59939 Human ant |
| C 39 | 19 | 95.0 | 23 | 8 | ABQ76994 | Abq76994 Human ant |
| C 40 | 19 | 95.0 | 23 | 8 | ACA94757 | ACA94757 Human sin |
| C 41 | 19 | 95.0 | 23 | 8 | ABX08571 | Abx08571 Human ant |
| C 42 | 19 | 95.0 | 23 | 8 | ADA49550 | Aad49550 Human VH |
| C 43 | 19 | 95.0 | 23 | 8 | ABX99235 | Abx99235 Anti-CAN- |
| C 44 | 19 | 95.0 | 23 | 8 | ACC48651 | Acc48651 Human ant |
| C 45 | 19 | 95.0 | 23 | 8 | ADQ54811 | Adq54811 Human TR4 |

ALIGNMENTS

RESULT 1
ABN84083
ID ABN84083 standard; DNA; 20 BP.
XX
AC ABN84083;
XX
DT 23-SBP-2002 (first entry)
XX
DE FRI collar sequence.
XX
KW Antibody; pRL5-CAT; vector; primer; ss.
XX
OS Unidentified.
XX
PN WO200246435-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US047452.
XX
PR 05-DEC-2000; 2000US-0251440P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
PI McWhirter J;
XX
DR WPI; 2002-537569/57.
XX
PT plasmid for in situ production of genes, comprises two template annealing
PT sequences, such as downstream primer and upstream collar sequence and a
PT restriction site located between the annealing sequences.
XX
PS Claim 36; Page 19; 65pp; English.
CC
CC The present sequence is an antibody framework region 1 (FRI) collar
CC oligonucleotide that is used in the engineering of plasmids of the
CC invention, especially plasmid pRL5-CAT (see ABN84083), for the in situ
CC production of genes. It was found nucleic acids encoding at least a
CC portion of an antibody can be directly incorporated into a plasmid by
CC reverse transcription of mRNA. The plasmid is engineered to contain 2
CC template annealing sequences, i.e. a downstream primer that anneals to a
CC first portion of a nucleic acid template, e.g. mRNA encoding at least a

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 498.992 Seconds
(without alignments)
1942.126 Million cell updates/sec

Title: US-10-006-591A-7

Perfect score: 20

Sequence: 1 gactgcaccagctgnacctg 20

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_btg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ets.*
- 12: gb_ey.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| C 2 | 19 | 95.0 | 20 | 6 | AX642155 Sequence |
| C 3 | 19 | 95.0 | 21 | 6 | AX740283 Sequence |
| C 4 | 19 | 95.0 | 22 | 6 | A38157 Sequence |
| C 5 | 19 | 95.0 | 23 | 6 | A27195 Sequence |
| C 6 | 19 | 95.0 | 23 | 6 | A32937 Sequence |
| C 7 | 19 | 95.0 | 23 | 6 | A33832 Sequence |
| C 8 | 19 | 95.0 | 23 | 6 | AR077341 Sequence |
| C 9 | 19 | 95.0 | 23 | 6 | AR117961 Sequence |
| C 10 | 19 | 95.0 | 23 | 6 | BD231855 Methods f |
| C 11 | 19 | 95.0 | 23 | 6 | CQ846560 Sequence |
| C 12 | 19 | 95.0 | 23 | 6 | E09108 Sequence |
| C 13 | 19 | 95.0 | 23 | 6 | I27516 Sequence |
| C 14 | 19 | 95.0 | 23 | 6 | I95682 Sequence |
| C 15 | 19 | 95.0 | 23 | 6 | AR265404 Sequence |
| C 16 | 19 | 95.0 | 23 | 6 | AR301925 Sequence |
| C 17 | 19 | 95.0 | 23 | 6 | AR428815 Sequence |
| C 18 | 19 | 95.0 | 23 | 6 | AR438217 Sequence |
| C 19 | 19 | 95.0 | 23 | 6 | AX010543 Sequence |

| | | | | | |
|------|----|------|----|---|--------------------|
| C 20 | 19 | 95.0 | 23 | 6 | AX357136 Sequence |
| C 21 | 19 | 95.0 | 23 | 6 | AX376780 Sequence |
| C 22 | 19 | 95.0 | 23 | 6 | AX795212 Sequence |
| C 23 | 19 | 95.0 | 36 | 6 | AX740338 Sequence |
| C 24 | 19 | 95.0 | 38 | 6 | A27204 Sequence |
| C 25 | 19 | 95.0 | 38 | 6 | A33845 Sequence |
| C 26 | 19 | 95.0 | 38 | 6 | I27529 Sequence |
| C 27 | 19 | 95.0 | 38 | 6 | AX658910 Sequence |
| C 28 | 19 | 95.0 | 39 | 6 | CQ879714 Sequence |
| C 29 | 19 | 95.0 | 39 | 6 | AX658939 Sequence |
| C 30 | 19 | 95.0 | 40 | 6 | CQ879694 Sequence |
| C 31 | 19 | 95.0 | 41 | 6 | AX190443 Sequence |
| C 32 | 19 | 95.0 | 41 | 6 | AX657269 Sequence |
| C 33 | 19 | 95.0 | 43 | 6 | AR454042 Sequence |
| C 34 | 19 | 95.0 | 44 | 6 | E11299 PCR primer |
| C 35 | 19 | 95.0 | 44 | 6 | AX175350 Sequence |
| C 36 | 19 | 95.0 | 45 | 6 | AR243937 Sequence |
| C 37 | 19 | 95.0 | 47 | 6 | CQ849429 Sequence |
| C 38 | 19 | 95.0 | 47 | 6 | AX004825 Sequence |
| C 39 | 19 | 95.0 | 47 | 6 | BD074255 Method fo |
| C 40 | 19 | 95.0 | 53 | 6 | AX376805 Sequence |
| C 41 | 19 | 95.0 | 53 | 6 | AX601773 Sequence |
| C 42 | 19 | 95.0 | 56 | 6 | A27390 Oligonucleo |
| C 43 | 19 | 95.0 | 56 | 6 | A32943 Synthetic p |
| C 44 | 19 | 95.0 | 56 | 6 | A33903 Synthetic p |
| C 45 | 19 | 95.0 | 56 | 6 | AR077347 Sequence |

ALIGNMENTS

RESULT 1
CQ874135/c
LOCUS CQ874135 20 bp DNA linear PAT 27-SEP-2004
DEFINITION Sequence 11 from Patent WO2004076620.
ACCESSION CQ874135
VERSION CQ874135.1 GI:52747700
KEYWORDS Homo sapiens. (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS van de Winkel J.G., van Dijk, M.A., Schuurman, J., Gerritsen, A.F., Baadsgaard, O.D. and Petersen, J.R.
TITLE Human antibodies specific for Interleukin 15 (il-15)
JOURNAL Patent: WO 2004076620-A 11 10-SEP-2004;
Genmab A/S (DK)

FEATURES
source Location/Qualifiers

1..20.
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 95.0%; Score 19; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACTGCACCAGCTGNACCTG 20

|||||
20 GACTGCACCAGCTGNACCTG 1

RESULT 2

AX642155
LOCUS AX642155 20 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7 from Patent WO0246435.
ACCESSION AX642155
VERSION AX642155.1 GI:28474643
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 459.664 seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-4
Perfect score: 50
Sequence: 1 attaacactctccctgttg.....tgacgggggaactcagggccc 50

Scoring table: IDENTITY NUC
Gapop.10.0 , Gapext 1.0

Searched: 5706582 seqs, 3073711274 residues
Total number of hits satisfying chosen parameters: 11413164

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA:
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
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15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 50 | 100.0 | 50 | 14 | US-10-006-591-4 |
| 2 | 50 | 100.0 | 68 | 14 | US-10-006-591-5 |
| 3 | 50 | 100.0 | 76 | 14 | US-10-006-591-6 |
| 4 | 50 | 100.0 | 357 | 9 | US-09-910-059-46 |
| 5 | 50 | 100.0 | 729 | 16 | US-10-016-986-152 |
| 6 | 50 | 100.0 | 729 | 16 | US-10-016-986-168 |
| 7 | 50 | 100.0 | 729 | 17 | US-10-010-907A-1 |
| 8 | 50 | 100.0 | 1539 | 18 | US-10-492-729-4 |
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| 10 | 48.4 | 96.8 | 724 | 9 | US-09-237-061-1 |
| 11 | 48.4 | 96.8 | 1081 | 9 | US-09-746-359A-20 |

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| C 12 | 48.4 | 96.8 | 1081 | 9 | US-09-951-268-21 | Sequence 21, Appl |
| C 13 | 48.4 | 96.8 | 1081 | 11 | US-09-745-792A-20 | Sequence 20, Appl |
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| C 15 | 48.4 | 96.8 | 1081 | 17 | US-10-471-151-27 | Sequence 27, Appl |
| C 16 | 48.4 | 96.8 | 2700 | 14 | US-10-227-694-3 | Sequence 3, Appl |
| C 17 | 48.4 | 96.8 | 2700 | 19 | US-10-754-212-1 | Sequence 1, Appl |
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| C 19 | 48.4 | 96.8 | 3000 | 19 | US-10-697-995-19 | Sequence 19, Appl |
| C 20 | 48.4 | 96.8 | 3100 | 14 | US-10-227-694-6 | Sequence 6, Appl |
| C 21 | 48.4 | 96.8 | 3100 | 19 | US-10-754-212-4 | Sequence 4, Appl |
| C 22 | 48.4 | 96.8 | 3242 | 19 | US-10-697-995-4 | Sequence 4, Appl |
| C 23 | 48.4 | 96.8 | 3255 | 19 | US-10-697-995-10 | Sequence 10, Appl |
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| C 25 | 48.4 | 96.8 | 3300 | 14 | US-10-020-786-2 | Sequence 2, Appl |
| C 26 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-4 | Sequence 4, Appl |
| C 27 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-6 | Sequence 6, Appl |
| C 28 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-8 | Sequence 8, Appl |
| C 29 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-10 | Sequence 10, Appl |
| C 30 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-12 | Sequence 12, Appl |
| C 31 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-20 | Sequence 20, Appl |
| C 32 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-22 | Sequence 22, Appl |
| C 33 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-24 | Sequence 24, Appl |
| C 34 | 48.4 | 96.8 | 3300 | 18 | US-10-764-428-26 | Sequence 26, Appl |
| C 35 | 48.4 | 96.8 | 3300 | 19 | US-10-697-995-1 | Sequence 1, Appl |
| C 36 | 48.4 | 96.8 | 3300 | 19 | US-10-697-995-7 | Sequence 7, Appl |
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| C 43 | 48.4 | 96.8 | 9182 | 10 | US-09-927-121B-89 | Sequence 89, Appl |
| C 44 | 48.4 | 96.8 | 10251 | 17 | US-10-045-674-582 | Sequence 582, App |
| C 45 | 48.4 | 96.8 | 13254 | 16 | US-10-016-986-156 | Sequence 156, App |

ALIGNMENTS

RESULT 1
US-10-006-591-4
; Sequence 4, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, Jehn
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-006-591-4

Query Match 100.0%; Score 50; DB 14; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTACACTCTCCCTGTGTGAGCTCTTTGTGACGGGCGAAGCTCAGGCC 50
DB 1 ATTACACTCTCCCTGTGTGAGCTCTTTGTGACGGGCGAAGCTCAGGCC 50

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:46:12 ; Search time 107.983 Seconds
(without alignments)
757.653 Million cell updates/sec

Title: US-10-006-591A-4
Perfect score: 50
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 4 | 50 | 100.0 | 646 | 5 | PCT-US94-01258-2 |
| C 5 | 50 | 100.0 | 646 | 5 | PCT-US95-11235-2 |
| C 6 | 50 | 100.0 | 729 | 1 | US-08-276-852-152 |
| C 7 | 50 | 100.0 | 729 | 1 | US-08-276-852-168 |
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| C 13 | 50 | 100.0 | 729 | 5 | PCT-US95-08743-168 |
| C 14 | 50 | 100.0 | 732 | 3 | US-08-860-882A-29 |
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| C 16 | 50 | 100.0 | 3217 | 3 | US-09-423-439-52 |
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| C 18 | 50 | 100.0 | 4691 | 3 | US-09-611-451-43 |
| C 19 | 50 | 100.0 | 6166 | 3 | US-08-591-632-51 |
| C 20 | 50 | 100.0 | 6166 | 3 | US-09-611-451-51 |
| C 21 | 48.4 | 96.8 | 724 | 4 | US-09-237-061-1 |
| C 22 | 48.4 | 96.8 | 1081 | 4 | US-09-746-359A-20 |
| C 23 | 48.4 | 96.8 | 5703 | 1 | US-08-467-420A-50 |
| C 24 | 48.4 | 96.8 | 5703 | 1 | US-08-470-110A-50 |
| C 25 | 48.4 | 96.8 | 5703 | 1 | US-08-667-769A-50 |
| C 26 | 48.4 | 96.8 | 5703 | 2 | US-08-940-371-50 |
| C 27 | 48.4 | 96.8 | 5703 | 3 | US-08-637-647-50 |

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|------|------|------|-------|---|--------------------|-------------------|
| C 28 | 48.4 | 96.8 | 5703 | 5 | PCT-US95-17082A-50 | Sequence 50, Appl |
| C 29 | 48.4 | 96.8 | 13254 | 1 | US-08-276-852-156 | Sequence 156, App |
| C 30 | 48.4 | 96.8 | 13254 | 1 | US-08-276-852-170 | Sequence 170, App |
| C 31 | 48.4 | 96.8 | 13254 | 1 | US-08-899-575-156 | Sequence 156, App |
| C 32 | 48.4 | 96.8 | 13254 | 1 | US-08-899-575-170 | Sequence 170, App |
| C 33 | 48.4 | 96.8 | 13254 | 1 | US-08-899-575-156 | Sequence 156, App |
| C 34 | 48.4 | 96.8 | 13254 | 1 | US-08-899-575-170 | Sequence 170, App |
| C 35 | 48.4 | 96.8 | 13254 | 5 | PCT-US95-08743-156 | Sequence 156, App |
| C 36 | 48.4 | 96.8 | 13254 | 5 | PCT-US95-08743-170 | Sequence 170, App |
| C 37 | 47.4 | 94.8 | 337 | 4 | US-10-134-188-27 | Sequence 27, Appl |
| C 38 | 47.4 | 94.8 | 714 | 1 | US-08-398-613A-27 | Sequence 27, Appl |
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| C 40 | 47.4 | 94.8 | 714 | 1 | US-08-398-611A-27 | Sequence 27, Appl |
| C 41 | 47.4 | 94.8 | 714 | 1 | US-08-396-851A-27 | Sequence 27, Appl |
| C 42 | 47.4 | 94.8 | 714 | 2 | US-08-491-334A-27 | Sequence 27, Appl |
| C 43 | 47.4 | 94.8 | 714 | 3 | US-09-027-44A-24 | Sequence 24, Appl |
| C 44 | 47.4 | 94.8 | 714 | 3 | US-08-804-444A-24 | Sequence 24, Appl |
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ALIGNMENTS

RESULT 1

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; Sequence 46, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, and Their Therapeutic Use in an Adept System
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-46

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Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 343 ATTACACTCTCCCTGTTGAAGCTTTTGTGACGGCGGAACCTCAGGCC 294

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; Sequence 2, Application US/08300386A
; Patent No. 5667988
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F, III
; APPLICANT: Burton, Dennis R
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
; TITLE OF INVENTION: USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 3062.6 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-4

Perfect score: 50

Sequence: 1 attaacactctccctgttg.....tgacggggaactcaggccc 50

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Searched: 34239544 seqs, 19032134700 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| c 34 | 46.8 | 93.6 | 366 | 2 | AA869615 |
| c 35 | 46.8 | 93.6 | 388 | 1 | AA485725 |
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ALIGNMENTS

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DEFINITION BE828579
ACCESSION BE828579
VERSION BE828579.1 GI:10260957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 246)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=et2=CM1-ET0043-030600-245-h06&t3=2000-06-03&t4=1)
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High quality sequence stop: 246.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqn2000s: *
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5: geneseqn2002s: *
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7: geneseqn2004s: *
8: geneseqn2005s: *
9: geneseqn2006s: *
10: geneseqn2007s: *
11: geneseqn2008s: *
12: geneseqn2009s: *
13: geneseqn2010s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 50 | 100.0 | 357 | 2 | AAV17287 |
| 5 | 50 | 100.0 | 646 | 2 | AAQ70487 |
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| 7 | 50 | 100.0 | 729 | 3 | AAQ70487 |
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| 14 | 50 | 100.0 | 1440 | 10 | ADP26475 |
| 15 | 50 | 100.0 | 1539 | 8 | ADP26475 |
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| C 37 | 48.4 | 96.8 | 3242 | 12 | ADO14124 |
| C 38 | 48.4 | 96.8 | 3255 | 12 | ADO14130 |
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| C 44 | 48.4 | 96.8 | 3300 | 13 | ADQ90720 |
| C 45 | 48.4 | 96.8 | 3300 | 13 | ADQ90702 |

ALIGNMENTS

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XX DT 23-SEP-2002 (first entry)
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XX KW Antibody; pRL5-CAT; vector; primer; ss.
XX OS Unidentified.
XX PN WO200246435-A2.
XX PD 13-JUN-2002.
XX PF 05-DEC-2001; 2001WO-US047452.
XX PR 05-DEC-2000; 2000US-0251440P.
XX PA (ALEX-) ALEXION PHARM INC.
XX PI Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;
XX PI McWhirter J;
XX DR WPI; 2002-537569/57.
XX PT Plasmid for in situ production of genes, comprises two template annealing
XX PT sequences, such as downstream primer and upstream collar sequence and a
XX PT restriction site located between the annealing sequences.
XX PS Claim 33; Page 18; 65pp; English.
XX CC The present sequence is an antibody kappa constant region primer that is
XX CC used in the engineering of plasmids of the invention, especially plasmid
XX CC pRL5-CAT (see ABN84078), for the in situ production of genes. It was
XX CC found nucleic acids encoding at least a portion of an antibody can be
XX CC directly incorporated into a plasmid by reverse transcription of mRNA.
XX CC The plasmid is engineered to contain 2 template annealing sequences, i.e.
XX CC a downstream primer that anneals to a first portion of a nucleic acid
XX CC template, e.g. mRNA encoding at least a portion of an antibody, and an

AAQ92546 pComb3 ex
AAQ92547 Expressio
ADO06855 Virucidal
ADO06857 Virucidal
AAQ90423 ChimERIC
AAH22820 Human IL-
AAH22820 Human IL-
ABK96181 DNA encod
AAD37589 Human IL-
AAD37589 Human IL-
ADJ83300 Human IL-
ADJ83300 Human IL-
ADZ82071 Dual-prom
ADO14135 Plasmid p
ADO14138 Plasmid p
ADZ82072 Dual-prom
ADO14124 Plasmid p
ADO14130 Plasmid p
ABN86646 Nucleotid
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ADO14127 Plasmid p
ADO14121 Plasmid p
ADQ90708 Anti-VEGF
ADQ90720 Anti-VEGF
ADQ90702 Anti-VEGF
ADQ90704 Anti-VEGF

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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ALIGNMENTS

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DEFINITION Sequence 4 from Patent WO0246435.
ACCESSION AX642152
VERSION AX642152.1 GI:28474640
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bowdish,K.S., Barbas-Frederickson,S., Lin,Y.C., Renshaw,M., Wild,M.
and McWhirter,J.
TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0246435-A 4 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

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Best Local Similarity 100.0%; Pred. No. 3.3e-09;
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Db 1 ATTAACACTCTCCCTGTGAGCTCTTTGTGACGGCGGAACCTCAGGCC 50
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RESULT 2
LOCUS AX642153/c 58 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5 from Patent WO0246435.
ACCESSION AX642153
VERSION AX642153.1 GI:28474641
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 4 | 50 | 100.0 | 357 | 6 | A67290 Sequence 46 |
| 5 | 50 | 100.0 | 357 | 6 | A94775 Sequence 19 |
| 6 | 50 | 100.0 | 634 | 9 | AJ810487 Macaca fa |
| 7 | 50 | 100.0 | 646 | 6 | AR105450 Sequence |
| 8 | 50 | 100.0 | 646 | 6 | I65403 Sequence 2 |
| 9 | 50 | 100.0 | 729 | 6 | AR038305 Sequence |
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| 17 | 50 | 100.0 | 2790 | 6 | AX744002 Sequence |
| 18 | 50 | 100.0 | 2810 | 6 | AX744006 Sequence |
| 19 | 50 | 100.0 | 3217 | 6 | A83232 Sequence 52 |

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 20:13:07 ; Search time 147.092 Seconds
(without alignments)
668.687 Million cell updates/sec

Title: US-10-006-591A-3

Perfect score: 16
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
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- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
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- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 15 | 93.8 | 20 | 9 | US-09-192-854-187 |
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| 4 | 15 | 93.8 | 20 | 9 | US-09-968-561A-325 |
| 5 | 15 | 93.8 | 20 | 9 | US-09-968-561A-337 |
| 6 | 15 | 93.8 | 20 | 10 | US-09-968-744A-325 |
| 7 | 15 | 93.8 | 20 | 10 | US-09-968-744A-337 |
| 8 | 15 | 93.8 | 20 | 11 | US-09-968-561A-325 |
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| 10 | 15 | 93.8 | 21 | 9 | US-09-810-999-1 |
| 11 | 15 | 93.8 | 21 | 10 | US-09-389-565-7 |

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| Sequence 14, Appl | 22 | 18 | US-10-485-466-14 | 93.8 | 15 | 17 | US-10-485-466-14 | 93.8 | 15 | 17 |
| Sequence 33, Appl | 23 | 9 | US-09-779-879A-33 | 93.8 | 15 | 18 | US-09-779-879A-33 | 93.8 | 15 | 18 |
| Sequence 31, Appl | 23 | 9 | US-09-025-403A-31 | 93.8 | 15 | 19 | US-09-025-403A-31 | 93.8 | 15 | 19 |
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| Sequence 48, Appl | 23 | 14 | US-10-075-846-48 | 93.8 | 15 | 36 | US-10-075-846-48 | 93.8 | 15 | 36 |
| Sequence 41, Appl | 23 | 14 | US-10-080-980-41 | 93.8 | 15 | 37 | US-10-080-980-41 | 93.8 | 15 | 37 |
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| Sequence 68, Appl | 23 | 14 | US-10-086-156-68 | 93.8 | 15 | 40 | US-10-086-156-68 | 93.8 | 15 | 40 |
| Sequence 38, Appl | 23 | 14 | US-10-081-775-38 | 93.8 | 15 | 41 | US-10-081-775-38 | 93.8 | 15 | 41 |
| Sequence 51, Appl | 23 | 14 | US-10-092-771-51 | 93.8 | 15 | 42 | US-10-092-771-51 | 93.8 | 15 | 42 |
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| Sequence 104, App | 23 | 14 | US-10-104-943-104 | 93.8 | 15 | 44 | US-10-104-943-104 | 93.8 | 15 | 44 |
| Sequence 150, App | 23 | 14 | US-10-120-604-150 | 93.8 | 15 | 45 | US-10-120-604-150 | 93.8 | 15 | 45 |

ALIGNMENTS

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; Sequence 3, Application US/10006591
; Publication No. US20030049731A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Renshaw, Mark
; APPLICANT: Wild, Martha
; APPLICANT: McWhirter, John
; TITLE OF INVENTION: ENGINEERED PLASMIDS AND THEIR USE FOR IN SITU PRODUCTION OF GEN.
; FILE REFERENCE: 1087-3
; CURRENT APPLICATION NUMBER: US/10/006,591
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/251,440
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: collar sequence
; NAME/KEY: misc feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: n is c o r t
US-10-006-591-3

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GenCore version 5.1.6
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757.653 Million cell updates/sec

Title: US-10-006-591A-3

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| C 6 | 15 | 93.8 | 20 | 4 | US-09-192-854-199 |
| C 7 | 15 | 93.8 | 21 | 3 | US-08-843-409-7 |
| C 8 | 15 | 93.8 | 21 | 4 | US-09-380-484A-2 |
| C 9 | 15 | 93.8 | 23 | 1 | US-08-211-202-72 |
| C 10 | 15 | 93.8 | 23 | 1 | US-08-388-672A-14 |
| C 11 | 15 | 93.8 | 23 | 3 | US-09-080-554-14 |
| C 12 | 15 | 93.8 | 23 | 3 | US-09-672-609-31 |
| C 13 | 15 | 93.8 | 23 | 3 | US-09-025-203-29 |
| C 14 | 15 | 93.8 | 23 | 3 | US-09-025-403A-31 |
| C 15 | 15 | 93.8 | 23 | 4 | US-10-067-443-43 |
| C 16 | 15 | 93.8 | 23 | 4 | US-09-999-021-29 |
| C 17 | 15 | 93.8 | 23 | 4 | US-09-999-025-29 |
| C 18 | 15 | 93.8 | 23 | 4 | US-10-040-997-29 |
| C 19 | 15 | 93.8 | 23 | 4 | US-09-999-040-29 |
| C 20 | 15 | 93.8 | 23 | 4 | US-09-998-817-29 |
| C 21 | 15 | 93.8 | 23 | 4 | US-09-726-219A-99 |
| C 22 | 15 | 93.8 | 24 | 4 | US-09-726-219A-59 |
| C 23 | 15 | 93.8 | 28 | 4 | US-09-726-219A-58 |
| C 24 | 15 | 93.8 | 31 | 4 | US-08-407-620A-39 |
| C 25 | 15 | 93.8 | 32 | 4 | US-08-454-899G-64 |
| C 26 | 15 | 93.8 | 32 | 4 | US-08-454-899G-65 |
| C 27 | 15 | 93.8 | 32 | 4 | US-09-726-219A-139 |
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Sequence 105, Appl
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Sequence 35, Appl
Sequence 54, Appl
Sequence 106, Appl
Sequence 372, Appl
Sequence 222, Appl
Sequence 1, Appl

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35 4 US-08-726-219A-145
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36 2 US-08-350-260A-91
36 2 US-08-350-260A-128
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36 4 US-09-104-337A-128
38 4 US-08-700-820C-8
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41 3 US-08-646-265A-105
43 3 US-08-832-985-54
43 3 US-09-410-903-35
43 4 US-08-835-159-54
44 3 US-08-646-265A-106
44 3 US-09-042-353-372
44 3 US-08-758-417A-222
45 4 US-09-602-263-1

ALIGNMENTS

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; Patent No. 5733743
; GENERAL INFORMATION:
; APPLICANT: Johnson, Kevin S
; APPLICANT: Winter, Gregory P
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Smith, Andrew JH
; APPLICANT: Waterhouse, P
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,619
; FILING DATE: 16-SEP-1994
; CLASSIFICATION: GOIN 33/531, GOIN 33/68
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REFERENCE/DOCKET NUMBER: 28111/32238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 18:38:52 ; Search time 980.034 Seconds
(without alignments)
621.436 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 gggctcatctggatgtn 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 3 | 15 | 93.8 | 141 | 2 | AW408234 |
| C 4 | 15 | 93.8 | 141 | 6 | CD692332 |
| C 5 | 15 | 93.8 | 142 | 6 | CD685432 |
| C 6 | 15 | 93.8 | 143 | 6 | CD690397 |
| C 7 | 15 | 93.8 | 159 | 7 | CV317632 |
| C 8 | 15 | 93.8 | 160 | 2 | AW610222 |
| C 9 | 15 | 93.8 | 166 | 4 | BM826867 |
| C 10 | 15 | 93.8 | 183 | 2 | AW405083 |
| C 11 | 15 | 93.8 | 184 | 6 | CA946304 |
| C 12 | 15 | 93.8 | 186 | 6 | CD704655 |
| C 13 | 15 | 93.8 | 188 | 6 | CD707547 |
| C 14 | 15 | 93.8 | 193 | 6 | CB986288 |
| C 15 | 15 | 93.8 | 195 | 1 | AA299576 |
| C 16 | 15 | 93.8 | 202 | 2 | AW407426 |
| C 17 | 15 | 93.8 | 202 | 6 | CD710370 |
| C 18 | 15 | 93.8 | 203 | 1 | AA295622 |
| C 19 | 15 | 93.8 | 203 | 6 | CD704895 |
| C 20 | 15 | 93.8 | 205 | 1 | AA360654 |
| C 21 | 15 | 93.8 | 208 | 2 | AW407280 |
| C 22 | 15 | 93.8 | 208 | 6 | CD692881 |
| C 23 | 15 | 93.8 | 208 | 6 | CD708211 |
| C 24 | 15 | 93.8 | 212 | 6 | CD707121 |

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|------|----|------|-----|---|----------|--------------------|
| 25 | 15 | 93.8 | 218 | 6 | CA946425 | CA946425 n105c07.x |
| c 26 | 15 | 93.8 | 220 | 6 | CD708863 | CD708863 EST25390 |
| c 27 | 15 | 93.8 | 223 | 2 | BE841882 | BE841882 MRI-ST009 |
| c 28 | 15 | 93.8 | 233 | 1 | AA327497 | AA327497 EST30844 |
| c 29 | 15 | 93.8 | 239 | 2 | BF876806 | BF876806 QV2-ET010 |
| c 30 | 15 | 93.8 | 240 | 6 | CD689881 | CD689881 EST6404.h |
| c 31 | 15 | 93.8 | 243 | 2 | AW405289 | AW405289 UI-HF-BLO |
| c 32 | 15 | 93.8 | 248 | 2 | AW404355 | AW404355 UI-HF-BLO |
| c 33 | 15 | 93.8 | 252 | 2 | AW407923 | AW407923 UI-HF-BLO |
| c 34 | 15 | 93.8 | 254 | 2 | AW406058 | AW406058 UI-HF-BLO |
| c 35 | 15 | 93.8 | 254 | 4 | BM825674 | BM825674 K-EST0097 |
| c 36 | 15 | 93.8 | 257 | 2 | BE720151 | BE720151 RC3-HT088 |
| c 37 | 15 | 93.8 | 257 | 6 | CD705199 | CD705199 EST21726 |
| c 38 | 15 | 93.8 | 262 | 4 | BM825712 | BM825712 K-EST0097 |
| c 39 | 15 | 93.8 | 266 | 6 | CD701383 | CD701383 EST17907 |
| c 40 | 15 | 93.8 | 266 | 6 | CD707453 | CD707453 EST23980 |
| c 41 | 15 | 93.8 | 267 | 8 | AQ629914 | AQ629914 RPT-11-4 |
| c 42 | 15 | 93.8 | 268 | 5 | BQ083770 | BQ083770 K-EST0146 |
| c 43 | 15 | 93.8 | 271 | 6 | CD708595 | CD708595 EST25122 |
| c 44 | 15 | 93.8 | 275 | 4 | BM826862 | BM826862 K-EST0099 |
| c 45 | 15 | 93.8 | 276 | 6 | CD686963 | CD686963 EST3484.h |

ALIGNMENTS

RESULT 1
CD704171/c

LOCUS CD704171 131 bp mRNA linear EST 25-JUN-2003
DEFINITION EST20698 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD704171

VERSION CD704171.1 GI:32234801

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: Yixin Zeng

Cancer Center

Sun Yat-sen University

651 Dongfeng Road East,

Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@zsuns.edu.cn.

Location/Qualifiers

1. .131

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="normal nasopharynx"

/clone_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match

Best Local Similarity

Matches 15; Conservative

93.8%; Score 15; DB 6; Length 131;

100.0%; Pred. No. 1.5e+03;

Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCATCTGGATGT 15

|||||

Db 101 GGGTCATCTGGATGT 87

RESULT 2

AW405292/c

LOCUS

DEFINITION

UI-HF-BLO-ack-a-04-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone

AW405292

133 bp mRNA linear EST 16-FEB-2000

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 13:55:57 ; Search time 118.185 Seconds
(without alignments)
801.421 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 ggcctcctcgatgtn 16
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 15 | 93.8 | 16 | 6 | ABN84079 |
| 2 | 15 | 93.8 | 18 | 2 | AAQ49011 |
| 3 | 15 | 93.8 | 20 | 2 | AAQ35949 |
| 4 | 15 | 93.8 | 20 | 2 | AAQ35937 |
| 5 | 15 | 93.8 | 21 | 2 | AAQ38487 |
| 6 | 15 | 93.8 | 21 | 2 | AAV48233 |
| 7 | 15 | 93.8 | 21 | 3 | AAZ47090 |
| 8 | 15 | 93.8 | 21 | 3 | AAA91851 |
| 9 | 15 | 93.8 | 21 | 6 | ABK13448 |
| 10 | 15 | 93.8 | 21 | 10 | ADQ03323 |
| 11 | 15 | 93.8 | 21 | 10 | ADQ03324 |
| 12 | 15 | 93.8 | 21 | 10 | ADQ03324 |
| 13 | 15 | 93.8 | 22 | 8 | ACA60812 |
| 14 | 15 | 93.8 | 23 | 2 | AAQ32314 |
| 15 | 15 | 93.8 | 23 | 2 | AAQ32314 |
| 16 | 15 | 93.8 | 23 | 2 | AAQ39375 |
| 17 | 15 | 93.8 | 23 | 2 | AAQ32405 |
| 18 | 15 | 93.8 | 23 | 2 | AAQ29183 |
| 19 | 15 | 93.8 | 23 | 2 | AAZ20999 |
| 20 | 15 | 93.8 | 23 | 2 | AAZ76629 |

| | | | | | | |
|------|----|------|----|---|----------|----------|
| C 21 | 15 | 93.8 | 23 | 4 | ABA03082 | Abn84079 |
| C 22 | 15 | 93.8 | 23 | 4 | AAQ49011 | Abn84079 |
| C 23 | 15 | 93.8 | 23 | 4 | AAQ35949 | Abn84079 |
| C 24 | 15 | 93.8 | 23 | 4 | AAQ35937 | Abn84079 |
| C 25 | 15 | 93.8 | 23 | 4 | AAQ38487 | Abn84079 |
| C 26 | 15 | 93.8 | 23 | 4 | AAV48233 | Abn84079 |
| C 27 | 15 | 93.8 | 23 | 4 | AAZ47090 | Abn84079 |
| C 28 | 15 | 93.8 | 23 | 4 | AAA91851 | Abn84079 |
| C 29 | 15 | 93.8 | 23 | 4 | ABK13448 | Abn84079 |
| C 30 | 15 | 93.8 | 23 | 4 | ADQ03323 | Abn84079 |
| C 31 | 15 | 93.8 | 23 | 4 | ADQ03324 | Abn84079 |
| C 32 | 15 | 93.8 | 23 | 4 | ADQ03324 | Abn84079 |
| C 33 | 15 | 93.8 | 23 | 4 | ACA60812 | Abn84079 |
| C 34 | 15 | 93.8 | 23 | 4 | AAQ32314 | Abn84079 |
| C 35 | 15 | 93.8 | 23 | 4 | AAQ32314 | Abn84079 |
| C 36 | 15 | 93.8 | 23 | 4 | AAQ39375 | Abn84079 |
| C 37 | 15 | 93.8 | 23 | 4 | AAQ32405 | Abn84079 |
| C 38 | 15 | 93.8 | 23 | 4 | AAQ29183 | Abn84079 |
| C 39 | 15 | 93.8 | 23 | 4 | AAZ20999 | Abn84079 |
| C 40 | 15 | 93.8 | 23 | 4 | AAZ76629 | Abn84079 |
| C 41 | 15 | 93.8 | 23 | 4 | AAQ49011 | Abn84079 |
| C 42 | 15 | 93.8 | 23 | 4 | AAQ35949 | Abn84079 |
| C 43 | 15 | 93.8 | 23 | 4 | AAQ35937 | Abn84079 |
| C 44 | 15 | 93.8 | 23 | 4 | AAQ38487 | Abn84079 |
| C 45 | 15 | 93.8 | 23 | 4 | AAV48233 | Abn84079 |

ALIGNMENTS

RESULT 1
ABN84079
ID ABN84079 standard; DNA; 16 BP.

AC ABN84079;

DT 23-SEP-2002 (first entry)

DE FRI collar sequence.

KW Antibody; pRL5-CAT; vector; primer; ss.

OS Unidentified.

PN WO200246435-A2.

PD 13-JUN-2002.

PF 05-DEC-2001; 2001WO-US047452.

PR 05-DEC-2000; 2000US-0251440P.

XX (ALEX-) ALEXION PHARM INC.

XX Bowdish KS, Barbas-Frederickson S, Lin Y, Renshaw M, Wild M;

XX McWhirter J;

XX WPI; 2002-537569/57.

XX Plasmid for in situ production of genes, comprises two template annealing sequences, such as downstream primer and upstream collar sequence and a restriction site located between the annealing sequences.

XX Claim 35; Page 18; 65pp; English.

XX The present sequence is an antibody framework region 1 (FRI) collar oligonucleotide that is used in the engineering of plasmids of the invention, especially plasmid pRL5-CAT (see ABN84078), for the in situ production of genes. It was found nucleic acids encoding at least a portion of an antibody can be directly incorporated into a plasmid 2 reverse transcription of mRNA. The plasmid is engineered to contain 2 template annealing sequences, i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a

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OM nucleic - nucleic search, using sw model

Run on: June 1, 2005, 16:29:42 ; Search time 399.193 Seconds
(without alignments)
1942.126 Million cell updates/sec

Title: US-10-006-591A-3
Perfect score: 16
Sequence: 1 gggcatctggtatgtn 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
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8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 15 | 93.8 | 16 | 6 | AX642151 Sequence |
| C 2 | 15 | 93.8 | 18 | 6 | AR077364 Sequence |
| C 3 | 15 | 93.8 | 18 | 6 | AR117984 Sequence |
| C 4 | 15 | 93.8 | 18 | 6 | I95705 Sequence 33 |
| C 5 | 15 | 93.8 | 18 | 6 | AR265427 Sequence |
| C 6 | 15 | 93.8 | 20 | 6 | AR476236 Sequence |
| C 7 | 15 | 93.8 | 20 | 6 | AR476248 Sequence |
| C 8 | 15 | 93.8 | 20 | 6 | BD077342 Method of |
| C 9 | 15 | 93.8 | 20 | 6 | BD077354 Method of |
| C 10 | 15 | 93.8 | 21 | 6 | AR105680 Sequence |
| C 11 | 15 | 93.8 | 21 | 6 | AR409374 Sequence |
| C 12 | 15 | 93.8 | 21 | 6 | AX306562 Sequence |
| C 13 | 15 | 93.8 | 21 | 6 | AX740319 Sequence |
| C 14 | 15 | 93.8 | 21 | 6 | AX740320 Sequence |
| C 15 | 15 | 93.8 | 21 | 6 | BD105911 Immunotox |
| C 16 | 15 | 93.8 | 23 | 6 | A27361 Oligonucleo |
| C 17 | 15 | 93.8 | 23 | 6 | A32955 Synthetic P |
| C 18 | 15 | 93.8 | 23 | 6 | A33874 Synthetic P |
| C 19 | 15 | 93.8 | 23 | 6 | A38167 Sequence 11 |

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| 20 | 15 | 93.8 | 23 | 6 | AR0438 Sequence 33 |
| 21 | 15 | 93.8 | 23 | 6 | AR0469 Sequence 29 |
| 22 | 15 | 93.8 | 23 | 6 | AR024223 Sequence |
| 23 | 15 | 93.8 | 23 | 6 | BD134033 Humanized |
| 24 | 15 | 93.8 | 23 | 6 | BD134914 High-affi |
| C 25 | 15 | 93.8 | 23 | 6 | BD169282 Degraded |
| C 26 | 15 | 93.8 | 23 | 6 | BD169393 Small rsm |
| C 27 | 15 | 93.8 | 23 | 6 | CQ846578 Sequence |
| C 28 | 15 | 93.8 | 23 | 6 | E09114 Synthetic o |
| C 29 | 15 | 93.8 | 23 | 6 | I27558 Sequence 72 |
| 30 | 15 | 93.8 | 23 | 6 | AR194447 Sequence |
| 31 | 15 | 93.8 | 23 | 6 | AR217969 Sequence |
| C 32 | 15 | 93.8 | 23 | 6 | AR301935 Sequence |
| C 33 | 15 | 93.8 | 23 | 6 | AR428825 Sequence |
| C 34 | 15 | 93.8 | 23 | 6 | AR438227 Sequence |
| 35 | 15 | 93.8 | 23 | 6 | AR535205 Sequence |
| 36 | 15 | 93.8 | 23 | 6 | AR535223 Sequence |
| 37 | 15 | 93.8 | 23 | 6 | AR559807 Sequence |
| 38 | 15 | 93.8 | 23 | 6 | AR560048 Sequence |
| 39 | 15 | 93.8 | 23 | 6 | AR560324 Sequence |
| C 40 | 15 | 93.8 | 23 | 6 | AX357146 Sequence |
| C 41 | 15 | 93.8 | 23 | 6 | AX376792 Sequence |
| C 42 | 15 | 93.8 | 23 | 6 | AX795224 Sequence |
| C 43 | 15 | 93.8 | 24 | 6 | A32920 Synthetic P |
| C 44 | 15 | 93.8 | 24 | 6 | CQ846538 Sequence |
| 45 | 15 | 93.8 | 28 | 6 | A31836 Synthetic P |

ALIGNMENTS

RESULT 1
AX642151 LOCUS AX642151 16 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3 from Patent WO0246435.
ACCESSION AX642151
VERSION AX642151.1 GI:28474639
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Bowdiah,K.S., Barbas-Frederickson,S., Lin,Y.C., Renshaw,M., Wild,M. and McWhirter,J.
TITLE Engineered plasmids and their use for in situ production of genes
JOURNAL Patent: WO 0246435-A 3 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
FEATURES
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="collar sequence"
misc_feature 16
/note="n is c or t"

ORIGIN
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Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCATCTGGATGT 15
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Db 1 GGGTCATCTGGATGT 15

RESULT 2
AR077364/c LOCUS AR077364 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 79 from patent US 5962255.
ACCESSION AR077364
VERSION AR077364.1 GI:10004110
KEYWORDS